

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 09/6008, 890A

Source: IFW/6

Date Processed by STIC: 4-14-05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 04/14/2005

PATENT APPLICATION: US/09/608,890A

TIME: 12:49:32

Input Set : A:\seqlist corr2.txt

Output Set: N:\CRF4\04142005\I608890A.raw

(pg. 6)

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3 <110> APPLICANT: Johnson, Gary L.
5 <120> TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To
6   External Signals
8 <130> FILE REFERENCE: CPI-004DVCP3CN
10 <140> CURRENT APPLICATION NUMBER: 09/608,890A
11 <141> CURRENT FILING DATE: 2000-06-30
13 <150> PRIOR APPLICATION NUMBER: 08/440,421
14 <151> PRIOR FILING DATE: 1995-05-15
16 <150> PRIOR APPLICATION NUMBER: 08/323,460
17 <151> PRIOR FILING DATE: 1994-10-14
19 <150> PRIOR APPLICATION NUMBER: 08/049,254
20 <151> PRIOR FILING DATE: 1993-04-15
22 <150> PRIOR APPLICATION NUMBER: 08/410,602
23 <151> PRIOR FILING DATE: 1995-03-24
25 <150> PRIOR APPLICATION NUMBER: 08/472,934
26 <151> PRIOR FILING DATE: 1995-06-06
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35 <213> ORGANISM: Mus musculus
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46 ctacagtgct ggaactctgc aagggccaag caggagagct ggcggttggg agagaaatac 180
48 ttaaagctgg gtccatcggg gttggtggtg tgcattacgt cttaagttgt atccttggaa 240
50 accaagctga atcaacaac tggcaagaac tgctgggtcg cctctgtctt atagacaggt 300
52 tgctgttgga atttctgtct gaattctatc ctcatattgt cagtactgat gtctcacaag 360
54 ctgagcctgt tgaaatcagg tacaagaagc tgctctcctt cttaaccttt gccttgcaat 420
56 ccattgacaa ttccactcg atggttgga agctctctcg gaggatatat ctgagctctg 480
58 ccagg atg gtg acc gca gtg ccc gct gtg ttt tcc aag ctg gta acc atg 530
59   Met Val Thr Ala Val Pro Ala Val Phe Ser Lys Leu Val, Thr Met
60       1           5           10           15
62 ctt aat gct tct ggc tcc acc cac ttc acc agg atg cgc cgg cgt ctg 578
63 Leu Asn Ala Ser Gly Ser Thr His Phe Thr Arg Met Arg Arg Arg Leu
64       20           25           30
66 atg gct atc gcg gat gag gta gaa att gcc gag gtc atc cag ctg ggt 626
67 Met Ala Ile Ala Asp Glu Val Glu Ile Ala Glu Val Ile Gln Leu Gly
68       35           40           45

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71 Val Glu Asp Thr Val Asp Gly His Gln Asp Ser Leu Gln Ala Val Ala
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74 ccc acc agc tgt cta gaa aac agc tcc ctt gag cac aca gtc cat aga 722
75 Pro Thr Ser Cys Leu Glu Asn Ser Ser Leu Glu His Thr Val His Arg
76      65      70      75
78 gag aaa act gga aaa gga cta agt gct acg aga ctg agt gcc agc tcg 770
79 Glu Lys Thr Gly Lys Gly Leu Ser Ala Thr Arg Leu Ser Ala Ser Ser
80 80      85      90      95
82 gag gac att tct gac aga ctg gcc ggc gtc tct gta gga ctt ccc agc 818
83 Glu Asp Ile Ser Asp Arg Leu Ala Gly Val Ser Val Gly Leu Pro Ser
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86 tca aca aca aca gaa caa cca aag cca gcg gtt caa aca aaa ggc aga 866
87 Ser Thr Thr Thr Glu Gln Pro Lys Pro Ala Val Gln Thr Lys Gly Arg
88      115      120      125
90 ccc cac agt cag tgt ttg aac tcc tcc cct ttg tct cat gct caa tta 914
91 Pro His Ser Gln Cys Leu Asn Ser Ser Pro Leu Ser His Ala Gln Leu
92      130      135      140
94 atg ttc cca gca cca tca gcc cct tgt tcc tct gcc ccg tct gtc cca 962
95 Met Phe Pro Ala Pro Ser Ala Pro Cys Ser Ser Ala Pro Ser Val Pro
96      145      150      155
98 gat att tct aag cac aga ccc cag gca ttt gtt ccc tgc aaa ata cct 1010
99 Asp Ile Ser Lys His Arg Pro Gln Ala Phe Val Pro Cys Lys Ile Pro
100 160      165      170      175
102 tcc gca tct cct cag aca cag cgc aag ttc tct cta caa ttc cag agg 1058
103 Ser Ala Ser Pro Gln Thr Gln Arg Lys Phe Ser Leu Gln Phe Gln Arg
104      180      185      190
106 aac tgc tct gaa cac cga gac tca gac cag ctc tcc cca gtc ttc act 1106
107 Asn Cys Ser Glu His Arg Asp Ser Asp Gln Leu Ser Pro Val Phe Thr
108      195      200      205
110 cag tca aga ccc cca ccc tcc agt aac ata cac agg cca aag cca tcc 1154
111 Gln Ser Arg Pro Pro Pro Ser Ser Asn Ile His Arg Pro Lys Pro Ser
112      210      215      220
114 cga ccc gtt ccg ggc agt aca agc aaa cta ggg gac gcc aca aaa agt 1202
115 Arg Pro Val Pro Gly Ser Thr Ser Lys Leu Gly Asp Ala Thr Lys Ser
116      225      230      235
118 agc atg aca ctt gat ctg ggc agt gct tcc agg tgt gac gac agc ttt 1250
119 Ser Met Thr Leu Asp Leu Gly Ser Ala Ser Arg Cys Asp Asp Ser Phe
120 240      245      250      255
122 ggc ggc ggc ggc aac agt ggc aac gcc gtc ata ccc agc gac gag aca 1298
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124      260      265      270
126 gtg ttc acg ccg gtg gag gac aag tgc agg tta gat gtg aac acc gag 1346
127 Val Phe Thr Pro Val Glu Asp Lys Cys Arg Leu Asp Val Asn Thr Glu
128      275      280      285
130 ctc aac tcc agc atc gag gac ctt ctt gaa gca tcc atg cct tca agt 1394
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134 gac acg aca gtc act ttc aag tcc gaa gtc gcc gtc ctc tct ccg gaa 1442

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138 aag gcc gaa aat gac gac acc tac aaa gac gac gtc aat cat aat caa      1490
139 Lys Ala Glu Asn Asp Asp Thr Tyr Lys Asp Asp Val Asn His Asn Gln
140 320                      325                      330                      335
142 aag tgc aaa gaa aag atg gaa gct gaa gag gag gag gct tta gcg atc      1538
143 Lys Cys Lys Glu Lys Met Glu Ala Glu Glu Glu Glu Ala Leu Ala Ile
144      340                      345                      350
146 gcc atg gcg atg tca gcg tct cag gat gcc ctc ccc atc gtc cct cag      1586
147 Ala Met Ala Met Ser Ala Ser Gln Asp Ala Leu Pro Ile Val Pro Gln
148      355                      360                      365
150 ctg cag gtg gaa aat gga gaa gat att atc atc att cag cag gac aca      1634
151 Leu Gln Val Glu Asn Gly Glu Asp Ile Ile Ile Ile Gln Gln Asp Thr
152      370                      375                      380
154 cca gaa act ctt cca gga cat acc aaa gcg aaa cag cct tac aga gaa      1682
155 Pro Glu Thr Leu Pro Gly His Thr Lys Ala Lys Gln Pro Tyr Arg Glu
156      385                      390                      395
158 gac gct gag tgg ctg aaa ggc cag cag ata ggc ctc gga gca ttt tct      1730
159 Asp Ala Glu Trp Leu Lys Gly Gln Gln Ile Gly Leu Gly Ala Phe Ser
160 400                      405                      410                      415
162 tcc tgt tac caa gca cag gat gtg ggg act ggg act tta atg gct gtg      1778
163 Ser Cys Tyr Gln Ala Gln Asp Val Gly Thr Gly Thr Leu Met Ala Val
164      420                      425                      430
166 aaa cag gtg acg tac gtc aga aac aca tcc tcc gag cag gag gag gtg      1826
167 Lys Gln Val Thr Tyr Val Arg Asn Thr Ser Ser Glu Gln Glu Glu Val
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170 gtg gaa gcg ttg agg gaa gag atc cgg atg atg ggt cac ctc aac cat      1874
171 Val Glu Ala Leu Arg Glu Glu Ile Arg Met Met Gly His Leu Asn His
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174 cca aac atc atc cgg atg ctg ggg gcc acg tgc gag aag agc aac tac      1922
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182 agt aaa tac gga gct ttc aag gag tca gtc gtc att aac tac act gag      2018
183 Ser Lys Tyr Gly Ala Phe Lys Glu Ser Val Val Ile Asn Tyr Thr Glu
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186 cag tta ctg cgt ggc ctt tcc tat ctc cac gag aac cag atc att cac      2066
187 Gln Leu Leu Arg Gly Leu Ser Tyr Leu His Glu Asn Gln Ile Ile His
188      515                      520                      525
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199 Thr Gly Ala Gly Glu Phe Gln Gly Gln Leu Leu Gly Thr Ile Ala Phe

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206 gta tgg agt gtt ggc tgc gcc att ata gaa atg gct tgt gca aaa cca 2306
207 Val Trp Ser Val Gly Cys Ala Ile Ile Glu Met Ala Cys Ala Lys Pro
208          595          600          605
210 cct tgg aat gca gaa aaa cac tcc aat cat ctc gcc ttg ata ttt aag 2354
211 Pro Trp Asn Ala Glu Lys His Ser Asn His Leu Ala Leu Ile Phe Lys
212          610          615          620
214 att gct agc gca act act gca ccg tcc atc ccg tca cac ctg tcc ccg 2402
215 Ile Ala Ser Ala Thr Thr Ala Pro Ser Ile Pro Ser His Leu Ser Pro
216          625          630          635
218 ggt ctg cgc gac gtg gcc gtg cgc tgc tta gaa ctt cag cct cag gac 2450
219 Gly Leu Arg Asp Val Ala Val Arg Cys Leu Glu Leu Gln Pro Gln Asp
220 640          645          650          655
222 cgg cct ccg tcc aga gag ctg ctg aaa cat ccg gtc ttc cgt acc acg 2498
223 Arg Pro Pro Ser Arg Glu Leu Leu Lys His Pro Val Phe Arg Thr Thr
224          660          665          670
226 tgg tagttaattg ttcagatcag ctctaattgga gacaggatat cgaaccggga 2551
227 Trp
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231 agccagaaac ggggccagcg gggaaccgta cctaagcatg tgattgacaa atcatgacct 2671
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235 cacaggactg gctctggggg accaggaagg cgatggagtt tgcattgacta aagaacagaa 2791
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245 tgtgttttta atgttatttg gtactcgaat tgtaaataac gtctactgct gtttattcca 3091
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249 aaattctacg tgctgtgtga ctatgactcc taagacttcc agggcttaag ggctaactcc 3211
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267 35 40 45
269 Glu Asp Thr Val Asp Gly His Gln Asp Ser Leu Gln Ala Val Ala Pro
270 50 55 60
272 Thr Ser Cys Leu Glu Asn Ser Ser Leu Glu His Thr Val His Arg Glu
273 65 70 75 80
275 Lys Thr Gly Lys Gly Leu Ser Ala Thr Arg Leu Ser Ala Ser Ser Glu

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287	Phe	Pro	Ala	Pro	Ser	Ala	Pro	Cys	Ser	Ser	Ala	Pro	Ser	Val	Pro	Asp
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290	Ile	Ser	Lys	His	Arg	Pro	Gln	Ala	Phe	Val	Pro	Cys	Lys	Ile	Pro	Ser
291				165				170				175				
293	Ala	Ser	Pro	Gln	Thr	Gln	Arg	Lys	Phe	Ser	Leu	Gln	Phe	Gln	Arg	Asn
294				180				185				190				
296	Cys	Ser	Glu	His	Arg	Asp	Ser	Asp	Gln	Leu	Ser	Pro	Val	Phe	Thr	Gln
297				195				200				205				
299	Ser	Arg	Pro	Pro	Pro	Ser	Ser	Asn	Ile	His	Arg	Pro	Lys	Pro	Ser	Arg
300				210				215				220				
302	Pro	Val	Pro	Gly	Ser	Thr	Ser	Lys	Leu	Gly	Asp	Ala	Thr	Lys	Ser	Ser
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309				260				265				270				
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312				275				280				285				
314	Asn	Ser	Ser	Ile	Glu	Asp	Leu	Leu	Glu	Ala	Ser	Met	Pro	Ser	Ser	Asp
315				290				295				300				
317	Thr	Thr	Val	Thr	Phe	Lys	Ser	Glu	Val	Ala	Val	Leu	Ser	Pro	Glu	Lys
318	305							310				315				320
320	Ala	Glu	Asn	Asp	Asp	Thr	Tyr	Lys	Asp	Asp	Val	Asn	His	Asn	Gln	Lys
321				325				330				335				
323	Cys	Lys	Glu	Lys	Met	Glu	Ala	Glu	Glu	Glu	Ala	Leu	Ala	Ile	Ala	
324				340				345				350				
326	Met	Ala	Met	Ser	Ala	Ser	Gln	Asp	Ala	Leu	Pro	Ile	Val	Pro	Gln	Leu
327				355				360				365				
329	Gln	Val	Glu	Asn	Gly	Glu	Asp	Ile	Ile	Ile	Ile	Gln	Gln	Asp	Thr	Pro
330				370				375				380				
332	Glu	Thr	Leu	Pro	Gly	His	Thr	Lys	Ala	Lys	Gln	Pro	Tyr	Arg	Glu	Asp
333	385							390				395				400
335	Ala	Glu	Trp	Leu	Lys	Gly	Gln	Gln	Ile	Gly	Leu	Gly	Ala	Phe	Ser	Ser
336				405				410				415				
338	Cys	Tyr	Gln	Ala	Gln	Asp	Val	Gly	Thr	Gly	Thr	Leu	Met	Ala	Val	Lys
339				420				425				430				
341	Gln	Val	Thr	Tyr	Val	Arg	Asn	Thr	Ser	Ser	Glu	Gln	Glu	Glu	Val	Val
342				435				440				445				
344	Glu	Ala	Leu	Arg	Glu	Glu	Ile	Arg	Met	Met	Gly	His	Leu	Asn	His	Pro
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347	Asn	Ile	Ile	Arg	Met	Leu	Gly	Ala	Thr	Cys	Glu	Lys	Ser	Asn	Tyr	Asn
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Please Note:

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The rules require that a line not exceed 72 characters in length. This includes spaces.

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Seq#:3; Line(s) 658,659,660,661,662,663,664,665,666,667,668,669,670,671,672
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Seq#:3; Line(s) 688,689,690,691,692,693,694,695,696,697,698,699,700,701,702
Seq#:3; Line(s) 703,704,705,706,707,708,709,710,711,712,713,714,715,716,717
Seq#:3; Line(s) 718,719,720,721,722,723,724,725,726,727,728,729,730,731,732
Seq#:3; Line(s) 733,734,735,736,737,738,739,740,741,742,743,744,745,746,747
Seq#:3; Line(s) 748,749,750,751,752,753,754,755,756,757,758,759,760,761,762
Seq#:3; Line(s) 763,764,765,766,767,768,769,770,771,772,773,774,775,776,777
Seq#:3; Line(s) 778,779,780,781,782,783,784,785,786,787,788,789,790,791,792

VERIFICATION SUMMARY

DATE: 04/14/2005

PATENT APPLICATION: US/09/608,890A

TIME: 12:49:33

Input Set : A:\seqlist corr2.txt

Output Set: N:\CRF4\04142005\I608890A.raw

L:2167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1061

M:341 Repeated in SeqNo=11

L:2416 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:112

L:3234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0

L:3256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0

L:3284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0